

J. Siew

ENTERED



1600

RAW SEQUENCE LISTING DATE: 06/14/2002
 PATENT APPLICATION: US/09/623,828C TIME: 15:08:23

Input Set : A:\50146.004002.SEQLIST.TXT
 Output Set: N:\CRF3\06142002\I623828C.raw

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4 <110> APPLICANT: Schweighoffer, Fabien
5      Bracco, Laurent
6      Tocque, Bruno
8 <120> TITLE OF INVENTION: Qualitative Differential Screening
11 <130> FILE REFERENCE: 50146/004002
13 <140> CURRENT APPLICATION NUMBER: 09/623,828C
14 <141> CURRENT FILING DATE: 2000-11-30
16 <150> PRIOR APPLICATION NUMBER: PCT/FR99/00547
17 <151> PRIOR FILING DATE: 1999-03-11
19 <160> NUMBER OF SEQ ID NOS: 16
21 <170> SOFTWARE: FastSEQ for Windows Version 4.0
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 23
25 <212> TYPE: DNA
26 <213> ORGANISM: Artificial Sequence
28 <220> FEATURE:
29 <223> OTHER INFORMATION: Synthetic
W--> 31 <221> NAME/KEY: misc_feature
32 <222> LOCATION: 13-19, 23
33 <223> OTHER INFORMATION: n = A,T,C or G
W--> 35 <400> 1
W--> 36 gagaagcggtt atnnnnnnna ggn                23
38 <210> SEQ ID NO: 2
39 <211> LENGTH: 24
40 <212> TYPE: DNA
41 <213> ORGANISM: Artificial Sequence
43 <220> FEATURE:
44 <223> OTHER INFORMATION: Synthetic
W--> 46 <221> NAME/KEY: misc_feature
47 <222> LOCATION: 13-20
48 <223> OTHER INFORMATION: n = A,T,C or G
W--> 50 <400> 2
W--> 51 gagaagcggtt atnnnnnnnn tccc                24
53 <210> SEQ ID NO: 3
54 <211> LENGTH: 23
55 <212> TYPE: DNA
56 <213> ORGANISM: Artificial Sequence
58 <220> FEATURE:
59 <223> OTHER INFORMATION: Synthetic
W--> 61 <221> NAME/KEY: misc_feature
62 <222> LOCATION: (13)...(23)
63 <223> OTHER INFORMATION: n = A,T,C or G
W--> 65 <400> 3

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W--> 66 gagaagcggtt atnnnnnnnn nnn                                23
    68 <210> SEQ ID NO: 4
    69 <211> LENGTH: 20
    70 <212> TYPE: DNA
    71 <213> ORGANISM: Artificial Sequence
    73 <220> FEATURE:
    74 <223> OTHER INFORMATION: Synthetic
W--> 76 <221> NAME/KEY: misc_feature
    77 <222> LOCATION: (13)...(17)
    78 <223> OTHER INFORMATION: n = A,T,C or G
W--> 80 <400> 4
W--> 81 gagaagcggtt atnnnnnncca                                20
    83 <210> SEQ ID NO: 5
    84 <211> LENGTH: 66
    85 <212> TYPE: DNA
    86 <213> ORGANISM: Artificial Sequence
    88 <220> FEATURE:
    89 <223> OTHER INFORMATION: Synthetic
    91 <400> SEQUENCE: 5
    92 ccacacctgg ccagtatgtg ctcaactggct tgcagagtgg gcagccagcc taagcatttg 60
    93 cactgg                                                                66
    95 <210> SEQ ID NO: 6
    96 <211> LENGTH: 23
    97 <212> TYPE: DNA
    98 <213> ORGANISM: Artificial Sequence
    100 <220> FEATURE:
    101 <223> OTHER INFORMATION: Synthetic
    103 <400> SEQUENCE: 6
    104 gggacctggt tgacatgaag ccc                                23
    106 <210> SEQ ID NO: 7
    107 <211> LENGTH: 22
    108 <212> TYPE: DNA
    109 <213> ORGANISM: Artificial Sequence
    111 <220> FEATURE:
    112 <223> OTHER INFORMATION: Synthetic
    114 <400> SEQUENCE: 7
    115 cagtttccgc tccacaggtt gc                                22
    117 <210> SEQ ID NO: 8
    118 <211> LENGTH: 96
    119 <212> TYPE: DNA
    120 <213> ORGANISM: Artificial Sequence
    122 <220> FEATURE:
    123 <223> OTHER INFORMATION: Synthetic
    125 <400> SEQUENCE: 8
    126 gtacgggaga gcacgaccac acctggccag tatgtgctca ctggcttgca gagtgggcag 60
    127 cctaagcatt tgctactggt ggacctgag ggtgtg                                96
    129 <210> SEQ ID NO: 9
    130 <211> LENGTH: 441
    131 <212> TYPE: PRT

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132 <213> ORGANISM: Artificial Sequence

134 <220> FEATURE:

135 <223> OTHER INFORMATION: Synthetic

137 <400> SEQUENCE: 9

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138 Met Asn Lys Leu Ser Gly Gly Gly Gly Arg Arg Thr Arg Val Glu Gly
139 1      5      10      15
140 Gly Gln Leu Gly Gly Glu Glu Trp Thr Arg His Gly Ser Phe Val Asn
141      20      25      30
142 Lys Pro Thr Arg Gly Trp Leu His Pro Asn Asp Lys Val Met Gly Pro
143      35      40      45
144 Gly Val Ser Tyr Leu Val Arg Tyr Met Gly Cys Val Glu Val Leu Gln
145      50      55      60
146 Ser Met Arg Ala Leu Asp Phe Asn Thr Arg Thr Gln Val Thr Arg Glu
147 65      70      75      80
148 Ala Ile Ser Leu Val Cys Glu Ala Val Pro Gly Ala Lys Gly Ala Thr
149      85      90      95
150 Arg Arg Arg Lys Pro Cys Ser Arg Pro Leu Ser Ser Ile Leu Gly Arg
151      100     105     110
152 Ser Asn Leu Lys Phe Ala Gly Met Pro Ile Thr Leu Thr Val Ser Thr
153      115     120     125
154 Ser Ser Leu Asn Leu Met Ala Ala Asp Cys Lys Gln Ile Ile Ala Asn
155      130     135     140
156 His His Met Gln Ser Ile Ser Phe Ala Ser Gly Gly Asp Pro Asp Thr
157 145     150     155     160
158 Ala Glu Tyr Val Ala Tyr Val Ala Lys Asp Pro Val Asn Gln Arg Ala
159      165     170     175
160 Cys His Ile Leu Glu Cys Pro Glu Gly Leu Ala Gln Asp Val Ile Ser
161      180     185     190
162 Thr Ile Gly Gln Ala Phe Glu Leu Arg Phe Lys Gln Tyr Leu Arg Asn
163      195     200     205
164 Pro Pro Lys Leu Val Thr Pro His Asp Arg Met Ala Gly Phe Asp Gly
165      210     215     220
166 Ser Ala Trp Asp Glu Glu Glu Glu Glu Pro Pro Asp His Gln Tyr Tyr
167 225     230     235     240
168 Asn Asp Phe Pro Gly Lys Glu Pro Pro Leu Gly Gly Val Val Asp Met
169      245     250     255
170 Arg Leu Arg Glu Gly Ala Ala Pro Gly Ala Ala Arg Pro Thr Ala Pro
171      260     265     270
172 Asn Ala Gln Thr Pro Ser His Leu Gly Ala Thr Leu Pro Val Gly Gln
173      275     280     285
174 Pro Val Gly Gly Asp Pro Glu Val Arg Lys Gln Met Pro Pro Pro Pro
175      290     295     300
176 Pro Cys Pro Gly Arg Glu Leu Phe Asp Asp Pro Ser Tyr Val Asn Val
177 305     310     315     320
178 Gln Asn Leu Asp Lys Ala Arg Gln Ala Val Gly Gly Ala Gly Pro Pro
179      325     330     335
180 Asn Pro Ala Ile Asn Gly Ser Ala Pro Arg Asp Leu Phe Asp Met Lys
181      340     345     350
182 Pro Phe Glu Asp Ala Leu Arg Val Pro Pro Pro Pro Gln Ser Val Ser

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183          355          360          365
184 Met Ala Glu Gln Leu Arg Gly Glu Pro Trp Phe His Gly Lys Leu Ser
185          370          375          380
186 Arg Arg Glu Ala Glu Ala Leu Leu Gln Leu Asn Gly Asp Phe Leu Val
187 385          390          395          400
188 Arg Thr Lys Asp His Arg Phe Glu Ser Val Ser His Leu Ile Ser Tyr
189          405          410          415
190 His Met Asp Asn His Leu Pro Ile Ile Ser Ala Gly Ser Glu Leu Cys
191          420          425          430
192 Leu Gln Gln Pro Val Glu Arg Lys Leu
193          435          440
196 <210> SEQ ID NO: 10
197 <211> LENGTH: 1326
198 <212> TYPE: DNA
199 <213> ORGANISM: Artificial Sequence
201 <220> FEATURE:
202 <223> OTHER INFORMATION: Synthetic
204 <400> SEQUENCE: 10
205 atgaacaagc tgagtggagg cggcggggcg aggactcggg tggagggggg ccagcttggg 60
206 ggcgaggagt ggacccgcca cgggagcttt gtcaataagc ccacgcgggg ctggctgcat 120
207 cccaacgaca agtcatggg acccggggtt tcctacttgg ttcggtacat gggttgtgtg 180
208 gaggtcctcc agtcaatgcg tgccctggac ttcaacaccc ggactcaggt caccagggag 240
209 gccatcagtc tgggtgtgtg ggtgtgtgcc ggtgctaagg gggcgacaag gaggagaaag 300
210 ccctgtagcc gcccgctcag ctctatcctg gggaggagta acctgaaatt tgctggaatg 360
211 ccaatcactc tcaccgtctc caccagcagc ctcaacctca tggccgcaga ctgcaaacag 420
212 atcatcgcca accaccacat gcaatctatc tcatttgcac ccggcgggga tccggacaca 480
213 gccgagtatg tcgcctatgt tgccaaagac cctgtgaatc agagagcctg ccacattctg 540
214 gagtgtcccg aagggttgc ccaggatgtc atcagcacca ttggccaggc cttcgagttg 600
215 cgcttcaaac aatacctcag gaaccacccc aaactggtca cccctcatga caggatggct 660
216 ggctttgatg gctcagcatg ggatgaggag gaggaagagc cacctgacca tcagtactat 720
217 aatgacttcc cggggaagga accccccttg gggggggttg tagacatgag gcttcgggaa 780
218 ggagccgctc caggggctgc tcgaccact gcacccaatg ccagacccc cagccacttg 840
219 ggagctacat tgcctgtagg acagcctgtt gggggagatc cagaagtccg caaacagatg 900
220 ccacctccac caccctgtcc aggcagagag ctttttgatg atccctccta tgtcaacgtg 960
221 cagaacctag acaaggccc gcaagcagtg ggtggtgctg ggccccccaa tctgtctatc 1020
222 aatggcagtg caccocggga cctgtttgac atgaagccct tcgaagatgc tcttcgggtg 1080
223 cctccacctc ccagtcggt gtccatggct gaggagctcc gaggggagcc ctggttccat 1140
224 gggaagctga gccggcggga ggtgagga ca ctgctgcagc tcaatgggga cttcttggtt 1200
225 cggactaagg atcacgctt tgaaagtgtc agtcacctta tcagctacca catggacaat 1260
226 cacttgccca tcctctctgc gggcagcgaa ctgtgtctac agcaacctgt ggagcggaaa 1320
227 ctgtga
229 <210> SEQ ID NO: 11
230 <211> LENGTH: 19
231 <212> TYPE: DNA
232 <213> ORGANISM: Artificial Sequence
234 <220> FEATURE:
235 <223> OTHER INFORMATION: Synthetic
237 <400> SEQUENCE: 11
238 tgcccaaatc aacaagagc

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RAW SEQUENCE LISTING

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Input Set : A:\50146.004002.SEQLIST.TXT

Output Set: N:\CRF3\06142002\I623828C.raw

240 <210> SEQ ID NO: 12
241 <211> LENGTH: 19
242 <212> TYPE: DNA
243 <213> ORGANISM: Artificial Sequence
245 <220> FEATURE:
246 <223> OTHER INFORMATION: Synthetic
248 <400> SEQUENCE: 12
249 ccctgacaa gcctgaata 19
251 <210> SEQ ID NO: 13
252 <211> LENGTH: 24
253 <212> TYPE: DNA
254 <213> ORGANISM: Artificial Sequence
256 <220> FEATURE:
257 <223> OTHER INFORMATION: Synthetic
259 <400> SEQUENCE: 13
260 atgtctcaga gcaaccggga gctg 24
262 <210> SEQ ID NO: 14
263 <211> LENGTH: 24
264 <212> TYPE: DNA
265 <213> ORGANISM: Artificial Sequence
267 <220> FEATURE:
268 <223> OTHER INFORMATION: Synthetic
270 <400> SEQUENCE: 14
271 gtggctccat tcaccgcggg gctg 24
273 <210> SEQ ID NO: 15
274 <211> LENGTH: 19
275 <212> TYPE: DNA
276 <213> ORGANISM: Artificial Sequence
278 <220> FEATURE:
279 <223> OTHER INFORMATION: Synthetic
281 <400> SEQUENCE: 15
282 tgccaagaag ggaaggagt 19
284 <210> SEQ ID NO: 16
285 <211> LENGTH: 20
286 <212> TYPE: DNA
287 <213> ORGANISM: Artificial Sequence
289 <220> FEATURE:
290 <223> OTHER INFORMATION: Synthetic
292 <400> SEQUENCE: 16
293 tgtcatgact ccagcaatag 20

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 06/14/2002
PATENT APPLICATION: US/09/623,828C TIME: 15:08:24

Input Set : A:\50146.004002.SEQLIST.TXT
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 13,14,15,16,17,18,19,23

Seq#:2; N Pos. 13,14,15,16,17,18,19,20

Seq#:3; N Pos. 13,14,15,16,17,18,19,20,21,22,23

Seq#:4; N Pos. 13,14,15,16,17

VERIFICATION SUMMARY

DATE: 06/14/2002

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Input Set : A:\50146.004002.SEQLIST.TXT

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L:31 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:35 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:1
L:36 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0
L:46 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:50 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:51 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:0
L:61 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:65 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:3
L:66 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
L:76 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:80 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:4
L:81 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0